

M. Rao

#11



RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/467,368

DATE: 09/17/2002
 TIME: 14:22:11

Input Set : N:\Crif3\RULE60\09467368.raw
 Output Set: N:\CRF4\09172002\I467368.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:
 5 (i) APPLICANT: Hansen, Peter Kamp
 6 Wagner, Peter
 7 Mullertz, Anette
 8 Knap, Inge Helmer
 10 (ii) TITLE OF INVENTION: Animal Feed Additives
 12 (iii) NUMBER OF SEQUENCES: 2
 14 (iv) CORRESPONDENCE ADDRESS:
 15 (A) ADDRESSEE: Novo Nordisk of North America, Inc.
 16 (B) STREET: 405 Lexington Avenue
 17 (C) CITY: New York
 18 (D) STATE: NY
 19 (E) COUNTRY: USA
 20 (F) ZIP: 10174
 22 (v) COMPUTER READABLE FORM:
 23 (A) MEDIUM TYPE: Diskette
 24 (B) COMPUTER: IBM Compatible
 25 (C) OPERATING SYSTEM: DOS
 26 (D) SOFTWARE: FastSEQ for Windows Version 2.0
 28 (vi) CURRENT APPLICATION DATA:
 C--> 29 (A) APPLICATION NUMBER: US/09/467,368
 C--> 30 (B) FILING DATE: 21-Dec-1999
 31 (C) CLASSIFICATION:
 34 (vii) PRIOR APPLICATION DATA:
 35 (A) APPLICATION NUMBER: US/08/886,765
 36 (B) FILING DATE: 1-JUL-1997
 38 (viii) ATTORNEY/AGENT INFORMATION:
 39 (A) NAME: Lambiris, Elias J
 40 (B) REGISTRATION NUMBER: 33,728
 41 (C) REFERENCE/DOCKET NUMBER: 4324.204-US
 43 (ix) TELECOMMUNICATION INFORMATION:
 44 (A) TELEPHONE: 212-867-0123
 45 (B) TELEFAX: 212-878-9655
 47 (2) INFORMATION FOR SEQ ID NO: 1:
 49 (i) SEQUENCE CHARACTERISTICS:
 50 (A) LENGTH: 983 base pairs
 51 (B) TYPE: nucleic acid
 52 (C) STRANDEDNESS: single
 53 (D) TOPOLOGY: linear
 55 (ii) MOLECULE TYPE: cDNA
 57 (vi) ORIGINAL SOURCE:
 58 (A) ORGANISM: Thermomyces lanuginosus

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59          (B) STRAIN: DSM 4109
61      (ix) FEATURE:
62          (A) NAME/KEY: CDS
63          (B) LOCATION:31..705
65      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
67 TCGGCCCCGAC GTCTTGCAAT CCTTGCAAGT ATG GTC GGC TTT ACC CCC GTT GCC      54
68                               Met Val Gly Phe Thr Pro Val Ala
69                               1               5
71 CTT GCG GCC TTA GCC GCG ACT GGG GCC CTG GCC TTC CCG GCA GGG AAT      102
72 Leu Ala Ala Leu Ala Ala Thr Gly Ala Leu Ala Phe Pro Ala Gly Asn
73      10               15               20
75 GCC ACG GAG CTC GAA AAG CGA CAG ACA ACC CCC AAC TCG GAG GGC TGG      150
76 Ala Thr Glu Leu Glu Lys Arg Gln Thr Thr Pro Asn Ser Glu Gly Trp
77      25               30               35               40
79 CAC GAT GGT TAT TAC TAT TCC TGG TGG AGT GAC GGT GGA GCG CAG GCC      198
80 His Asp Gly Tyr Tyr Tyr Ser Trp Trp Ser Asp Gly Gly Ala Gln Ala
81               45               50               55
83 ACG TAC ACC AAC CTG GAA GGC GGC ACC TAC GAG ATC AGC TGG GGA GAT      246
84 Thr Tyr Thr Asn Leu Glu Gly Gly Thr Tyr Glu Ile Ser Trp Gly Asp
85               60               65               70
87 GGC GGT AAC CTC GTC GGT GGA AAG GGC TGG AAC CCC GGC CTG AAC GCA      294
88 Gly Gly Asn Leu Val Gly Gly Lys Gly Trp Asn Pro Gly Leu Asn Ala
89               75               80               85
91 AGA GCC ATC CAC TTT GAG GGT GTT TAC CAG CCA AAC GGC AAC AGC TAC      342
92 Arg Ala Ile His Phe Glu Gly Val Tyr Gln Pro Asn Gly Asn Ser Tyr
93      90               95               100
95 CTT GCG GTC TAC GGT TGG ACC CGC AAC CCG CTG GTC GAG TAT TAC ATC      390
96 Leu Ala Val Tyr Gly Trp Thr Arg Asn Pro Leu Val Glu Tyr Tyr Ile
97      105               110               115               120
99 GTC GAG AAC TTT GGC ACC TAT GAT CCT TCC TCC GGT GCT ACC GAT CTA      438
100 Val Glu Asn Phe Gly Thr Tyr Asp Pro Ser Ser Gly Ala Thr Asp Leu
101               125               130               135
103 GGA ACT GTC GAG TGC GAC GGT AGC ATC TAT CGA CTC GGC AAG ACC ACT      486
104 Gly Thr Val Glu Cys Asp Gly Ser Ile Tyr Arg Leu Gly Lys Thr Thr
105               140               145               150
107 CGC GTC AAC GCA CCT AGC ATC GAC GGC ACC CAA ACC TTC GAC CAA TAC      534
108 Arg Val Asn Ala Pro Ser Ile Asp Gly Thr Gln Thr Phe Asp Gln Tyr
109               155               160               165
111 TGG TCG GTC CGC CAG GAC AAG CGC ACC AGC GGT ACC GTC CAG ACG GGC      582
112 Trp Ser Val Arg Gln Asp Lys Arg Thr Ser Gly Thr Val Gln Thr Gly
113      170               175               180
115 TGC CAC TTC GAC GCC TGG GCT CGC GCT GGT TTG AAT GTC AAC GGT GAC      630
116 Cys His Phe Asp Ala Trp Ala Arg Ala Gly Leu Asn Val Asn Gly Asp
117      185               190               195               200
119 CAC TAC TAC CAG ATC GTT GCA ACG GAG GGC TAC TTC AGC AGC GGC TAT      678
120 His Tyr Tyr Gln Ile Val Ala Thr Glu Gly Tyr Phe Ser Ser Gly Tyr
121               205               210               215
123 GCT CGC ATC ACC GTT GCT GAC GTG GGC TAAGACGTAA CCTGGTGGTG      725
124 Ala Arg Ile Thr Val Ala Asp Val Gly

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125          220          225
127 ATCTCGCGAG GCAACAGCCA AGAATGTCGT CAGATGTGCC GGTGAAGGT ATTCAATCAG 785
129 CATATCTGTC TGCCCTTGCG AGTGATACTT TGGAGGACTG TGGAGAACTT TGTGCGAGCC 845
131 TGGCCAGGAT CAGTAGTTGC TTTGCGGTGT TTTGCTCCCT ATTCTCGTGA AAAAATTGTT 905
133 ATTGCTTCGT TGTCTAGTGT ACATAGCCGA GCAATTGAGG CCTCACGCTT GGGAAAAAAA 965
135 AAAAAAAAAA AAAAAAAAAA 983
137 (2) INFORMATION FOR SEQ ID NO: 2:
139 (i) SEQUENCE CHARACTERISTICS:
140 (A) LENGTH: 225 amino acids
141 (B) TYPE: amino acid
142 (D) TOPOLOGY: linear
144 (ii) MOLECULE TYPE: protein
146 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
148 Met Val Gly Phe Thr Pro Val Ala Leu Ala Ala Leu Ala Ala Thr Gly
149 1 5 10 15
151 Ala Leu Ala Phe Pro Ala Gly Asn Ala Thr Glu Leu Glu Lys Arg Gln
152 20 25 30
154 Thr Thr Pro Asn Ser Glu Gly Trp His Asp Gly Tyr Tyr Tyr Ser Trp
155 35 40 45
157 Trp Ser Asp Gly Gly Ala Gln Ala Thr Tyr Thr Asn Leu Glu Gly Gly
158 50 55 60
160 Thr Tyr Glu Ile Ser Trp Gly Asp Gly Gly Asn Leu Val Gly Gly Lys
161 65 70 75 80
163 Gly Trp Asn Pro Gly Leu Asn Ala Arg Ala Ile His Phe Glu Gly Val
164 85 90 95
166 Tyr Gln Pro Asn Gly Asn Ser Tyr Leu Ala Val Tyr Gly Trp Thr Arg
167 100 105 110
169 Asn Pro Leu Val Glu Tyr Tyr Ile Val Glu Asn Phe Gly Thr Tyr Asp
170 115 120 125
172 Pro Ser Ser Gly Ala Thr Asp Leu Gly Thr Val Glu Cys Asp Gly Ser
173 130 135 140
175 Ile Tyr Arg Leu Gly Lys Thr Thr Arg Val Asn Ala Pro Ser Ile Asp
176 145 150 155 160
178 Gly Thr Gln Thr Phe Asp Gln Tyr Trp Ser Val Arg Gln Asp Lys Arg
179 165 170 175
181 Thr Ser Gly Thr Val Gln Thr Gly Cys His Phe Asp Ala Trp Ala Arg
182 180 185 190
184 Ala Gly Leu Asn Val Asn Gly Asp His Tyr Tyr Gln Ile Val Ala Thr
185 195 200 205
187 Glu Gly Tyr Phe Ser Ser Gly Tyr Ala Arg Ile Thr Val Ala Asp Val
188 210 215 220
190 Gly
191 225

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VERIFICATION SUMMARY

DATE: 09/17/2002

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TIME: 14:22:12

Input Set : N:\Crf3\RULE60\09467368.raw

Output Set: N:\CRF4\09172002\I467368.raw

L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]